

REPLACEMENT SHEET



Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	1	5	10	15
Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	20	25	30	
Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	35	40	45	
Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	50	55	60	
Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	65	70	75	80
Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	85	90	95	
Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	100	105	110	
Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	115	120	125	
Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	130	135	140	
Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	145	150	155	160
Cys	Arg	Thr	Gly	Asp	165														

FIG. 1

REPLACEMENT SHEET

Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	
1				5					10					15		
Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	
			20					25					30			
Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	
		35					40					45				
Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	
	50					55					60					
Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	
65					70					75					80	
Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	
				85					90					95		
Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	
			100					105					110			
Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	
		115					120					125				
Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	
	130					135					140					
Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	
145					150					155					160	
Cys	Arg	Thr	Gly	Asp	Arg											
				165												

FIG. 2

REPLACEMENT SHEET

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GGAATTCACCACCATGGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCT
1  -----+-----+-----+-----+-----+-----+ 60
CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCGACACCGAAGAGGACAGGGA
      M G V H E C P A W L W L L L S L -
GCTGTCGCTCCCTCTGGGCCTCCCAGTCTGGGCGCCCCCCCCCGAATCGAGGGCCGCGC
61  -----+-----+-----+-----+-----+-----+ 120
CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCGCGGGGGGGGGCTTAGCTCCCGGCGCG
      L S L P L G L P V L G A P P R I E G R A -
CCCACCACGCCTCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAGGA
121 -----+-----+-----+-----+-----+-----+ 180
GGGTGGTGGGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCCT
      P P R L I C D S R V L E R Y L L E A K E -
GGCCGAGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGT
181 -----+-----+-----+-----+-----+-----+ 240
CCGGCTCTTATAGTGCTGCCCGACACGACTTGTGACGTGCAACTTACTCTTATAGTGACA
      A E N I T T G C A E H C S L N E N I T V -
CCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGATGGAGGTCGGGCAGCAGGCCGT
241 -----+-----+-----+-----+-----+-----+ 300
GGGTCTGTGGTTTCAATTAAAGATACGGACCTTCTCCTACCTCCAGCCCGTCGTCCGGCA
      P D T K V N F Y A W K R M E V G Q Q A V -
AGAAGTCTGGCAGGGCCTGGCCCTGCTGTGCGGAAGCTGTCTGCGGGGCCAGGCCCTGTT
301 -----+-----+-----+-----+-----+-----+ 360
TCTTCAGACCGTCCCGGACCGGGACGACAGCCTTCGACAGGACGCCCCGGTCCGGGACAA
      E V W Q G L A L L S E A V L R G Q A L L -
GGTCAACTCTTCCCAGCCGTGGGAGCCCCGTCAGCTGCATGTGGATAAAGCCGTCAGTGG
361 -----+-----+-----+-----+-----+-----+ 420
CCAGTTGAGAAGGGTCGGCACCCCTCGGGGACGTCGACGTACACCTATTTGCGCAGTCACC
      V N S S Q P W E P L Q L H V D K A V S G -
CCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGGGAGCCAGAAGGAAGCCATCTCCCC
421 -----+-----+-----+-----+-----+-----+ 480
GGAAGCGTCGGAGTGGTGAGACGAAGCCCGAGACCCTCGGGTCTTCCTTCGGTAGAGGGG

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FIG. 3a

REPLACEMENT SHEET

L R S L T T L L R A L G A Q K E A I S P -
 TCCAGATGCGGCCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCCGCAAACT
 481 -----+-----+-----+-----+-----+-----+ 540
 AGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTTAGTGACGACTGTGAAAGGCGTTTGA
 P D A A S A A P L R T I T A D T F R K L -
 CTTCCGAGTCTACTCCAATTTCTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTG
 541 -----+-----+-----+-----+-----+-----+ 600
 GAAGGCTCAGATGAGGTTAAAGGAGGCCCTTTTCGACTTCGACATGTGTCCCCTCCGGAC
 F R V Y S N F L R G K L K L Y T G E A C -
 CAGGACAGGGGACAGATGACCAGGTCGAC
 601 -----+-----+-----+-----+ 629
 GTCCTGTCCCCTGTCTACTGGTCCAGCTG
 R T G D R * -

FIG. 3b

REPLACEMENT SHEET

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1  GGAATTCACCACCATGGGGGTGCACGAATGTCTGCCTGGCTGTGGCTTCTCCTGTCCCT
   -----+-----+-----+-----+-----+ 60
   CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCGACACCGAAGAGGACAGGGA
       M G V H E C P A W L W L L S L -
61  GCTGTCGCTCCCTCTGGGCCTCCCAGTCTGCGCGCCCCCCCCGCCCCACCACGCCTCAT
   -----+-----+-----+-----+-----+ 120
   CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCGCGGGGGGGCGGGGTGGTGCGGAGTA
       L S L P L G L P V L G A P P A P P R L I -
121 CTGTGACAGCCGAGTCCTGGAGAGGTACCTCTTGAGAGCCAAGGAGGCCGAGAATATCAC
   -----+-----+-----+-----+-----+ 180
   GACACTGTGCGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCCTCCGGCTCTTATAGTG
       C D S R V L E R Y L L E A K E A E N I T -
181 GACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGTCCAGACACCAAAGT
   -----+-----+-----+-----+-----+ 240
   CTGCCCCGACACGACTTGTGACGTGCACTTACTCTTATAGTGACAGGGTCTGTGGTTTCA
       T G C A E H C S L N E N I T V P D T K V -
241 TAATTTCTATGCCTGGAAGAGGATGGAGGTCGGGCAGCAGGCCGTAGAACTCTGGCAGGG
   -----+-----+-----+-----+-----+ 300
   ATTAAAGATACGGACCTTCTCCTACCTCCAGCCCGTCGTCCGGCATCTTCAGACCGTCCC
       N F Y A W K R M E V G Q Q A V E V W Q G -
301 CCTGGCCCTGCTGTGCGAAGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCCCA
   -----+-----+-----+-----+-----+ 360
   GGACCGGGACGACAGCCTTCGACAGGACGCCCCGGTCCGGGACAACCACTTGAGAAGGGT
       L A L L S E A V L R G Q A L L V N S S Q -
361 GCCGTGGGAGCCCCTGCAGCTGCATGTGGATAAAGCCGTAGTGGCCTTCGCAGCCTCAC
   -----+-----+-----+-----+-----+ 420
   CGGCACCCTCGGGGACGTGACGTACACCTATTTCCGGCAGTCACCGGAAGCGTCGGAGTG
       P W E P L Q L H V D K A V S G L R S L T -
421 CACTCTGCTTCGGGCTCTGGGAGCCCAGAAGGAAGCCATCTCCCCTCCAGATGCGGCCTC
   -----+-----+-----+-----+-----+ 480
   GTGAGACGAAGCCCGAGACCCTCGGGTCTTCCTTCGGTAGAGGGGAGGTCTACGCCGGAG
       T L L R A L G A Q K E A I S P P D A A S -

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FIG. 4a

REPLACEMENT SHEET

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AGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCGCAAACCTCTTCCGAGTCTACTC
481 -----+-----+-----+-----+-----+-----+ 540
TCGACGAGGTGAGGCTTGTTAGTGACGACTGTGAAAGGCGTTTGAGAAGGCTCAGATGAG
  A A P L R T I T A D T F R K L F R V Y S -

CAATTCCTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAGGGGACAG
541 -----+-----+-----+-----+-----+-----+ 600
GTTAAAGGAGGCCCTTTCGACTTCGACATGTGTCCCCTCCGGACGTCCTGTCCCCTGTC
  N F L R G K L K L Y T G E A C R T G D R -

ATGACCAGGTCGAC
601 -----+----- 614
TACTGGTCCAGCTG
  * -

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FIG. 4b

REPLACEMENT SHEET

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GGAATTCACCACCATGGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCT
1  -----+-----+-----+-----+-----+-----+ 60
CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCGACACCGAAGAGGACAGGGA
      M G V H E C P A W L W L L L S L -
GCTGTCGCTCCCTCTGGGCCTCCCAGTCCTGGGCGCCCCCCCCCGGCGCCGCCCCTACGC
61  -----+-----+-----+-----+-----+-----+ 120
CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCGCGGGGGGGGCGCGGGCGGGTGATGCG
      L S L P L G L P V L G A P P G A A H Y A -
CCCACCACGCCTCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTCTTGAGGCCAAGGA
121 -----+-----+-----+-----+-----+-----+ 180
GGGTGGTGCAGGAGTAGACACTGTGCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCCT
      P P R L I C D S R V L E R Y L L E A K E -
GGCCGAGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGT
181 -----+-----+-----+-----+-----+-----+ 240
CCGGCTCTTATAGTGTGCGGACACGACTTGTGACGTCGAACCTACTCTTATAGTGACA
      A E N I T T G C A E H C S L N E N I T V -
CCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGATGGAGGTCGGGCAGCAGGCCGT
241 -----+-----+-----+-----+-----+-----+ 300
GGGTCTGTGGTTTCAATTAAAGATACGGACCTTCTCCTACCTCCAGCCCGTCGTCGGGCA
      P D T K V N F Y A W K R M E V G Q Q A V -
AGAAGTCTGGCAGGGCCTGGCCCTGCTGTGCGGAAGCTGTCCTGCGGGGCCAGGCCCTGTT
301 -----+-----+-----+-----+-----+-----+ 360
TCTTCAGACCGTCCCGGACCGGGACGACAGCCTTCGACAGGACGCCCCGGTCCGGGACAA
      E V W Q G L A L L S E A V L R G Q A L L -
GGTCAACTCTTCCCAGCCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG
361 -----+-----+-----+-----+-----+-----+ 420
CCAGTTGAGAAGGGTCGGCACCCCTCGGGGACGTCGACGTACACCTATTTCCGCAGTCACC
      V N S S Q P W E P L Q L H V D K A V S G -
CCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGGGAGCCCAGAAGGAAGCCATCTCCCC
421 -----+-----+-----+-----+-----+-----+ 480
GGAAGCGTCGGAGTGGTGAGACGAAGCCCAGACCCCTCGGGTCTTCCTTCGGTAGAGGGG
      L R S L T T L L R A L G A Q K E A I S P -

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FIG. 5a

REPLACEMENT SHEET

TCCAGATGCGGCCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCGCAAAC
481 -----+-----+-----+-----+-----+-----+ 540
AGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTTAGTGACGACTGTGAAAGGCGTTTGA
P D A A S A A P L R T I T A D T F R K L -

CTTCCGAGTCTACTCCAATTTCTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTG
541 -----+-----+-----+-----+-----+-----+ 600
GAAGGCTCAGATGAGGTAAAGGAGGCCCTTTCGACTTCGACATGTGTCCCCTCCGGAC
F R V Y S N F L R G K L K L Y T G E A C -

CAGGACAGGGGACAGATGACCAGGTCGAC
601 -----+-----+-----+-----+ 629
GTCCTGTCCCCTGTCTACTGGTCCAGCTG
R T G D R * -

FIG. 5b